SEQUENCE LISTING

<110> Hosted, Jr., Thomas J.
      Horan, Ann C.

<120> Isolation of Micromonospora carbonacea var africana
      pMLP1 integrase and use of integrating function for
      site-specific integration into Micromonospora
      halophitica and Micromonospora carbonacea chromosome

<130> IN01164K

<140> 09/855,340
<141> May 15, 2001

<150> 60/204,670
<151> 2000-05-17

<160> 16

<170> PatentIn Ver. 2.1

<210> 1
<211> 1179
<212> DNA
<213> Micromonospora carbonacea

<400> 1
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gtcaccattc agaccggtta tccgacgaag accagcgcca agaatgcgat ggtgcagttc 120
cgtgcggagc agttgcaggg caacgcgctc atgccgcgcg gcggtcagat taccctcgcc 180
gatttcgtgg gggagtggtg gccgagctac gaaaagacgc tgaaaccgac cgccgtgaac 240
tcggagggca accggatccg caaccacctc ctgcccatac tcggccatct caccettgac 300
gagctggacg ggcaggtcac ccagcagtgg gtcaacgacc tggaggccgg cgtcggcccg 360
tggccggagt ccacgcgggg tcgtcggaag ccgctggcag cgaagacgat cagcaactgc 420
cacggcctgc tgcacacgat ctgcggcgcg gcgatcgcgg cgaaacggat caggctcaac 480
ccgtgctctt cgacgatgct gccccggcgc gagccgaaag agatgaagtt cctgagcgac 540
ccggagatcg gtcggcttat cacggcgctt ccgccgcact ggcgaccgct cgtcatgctg 600
ctggtggcga ccggtctgag gtggggtgag gcgatcggcc tgcgcgccgg ccgggtcgac 660
ctgctcgccg cgcggccccg gctgaccgtc gtcgagcagc tccaggagct ggccagcacg 720
ggagagctcg tcttccagtc gccgaagacc gcgaagggcc ggcgcacggt cagtttcacc 780
acgaaagtcg ctctactgct tacgccactc atcgccggaa agaaaagtga cgaggtcgtg 840
ttcaccgcgc cgaaaggcgg gatggtaagg acgcgcaatt ccggcggat ctgggtcaag 900
gcgtgcgagg aagccgggct tccgggctta cgcattcacg atctgcggca cactcacgcg 960
gcgatcctga tttctgccgg gcgtccgctg tcggcgatct cccgccgcct cggtcactcg 1020
tcgatcgcgg tcacggatct gctgtacggg cacctgcgtg aggaggtcga cgagggatc 1080
ctcgcggcga tcgaggaggc gatggccggc gtccgggctg aggacctgga ggcggaactc 1140
gacgaggagc tgacggacgt gttggccgac gcagcatga 1179

<210> 2
<211> 426
<212> DNA
<213> Micromonospora carbonacea

<400> 2
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gagcgcgccg gactgaccaa gagcgagttg gccaggcgca tccagaagga ccgggccacc 120
gtcggccggt gggaggacgg caagaaccgg cccgacgacg cggacctcgt tgcccgcgtc 180
gcccaggtgc tcggcctcga cctcgacgaa gccctcgccg ccgcaggtct gcgccccggc 240
gtcaccccgc cagcgacccc aaccatggac ctggacgagg aaatcgagct ggtccgcacc 300

gaccccaagc tggacgagga càtgaagcgg cgcatcatcg ccctaatcct ggagcgccgt 360
gagcgcgaca aggcggcggc gatcgaggaa accaagcggc tcatcgacct gttccgccgg 420
agctga   426

<210> 3
<211> 34
<212> DNA
<213> Micromonospora carbonacea

<400> 3
ccccggtacg ggttcaattc ccatcagtca cccg   34

<210> 4
<211> 241
<212> DNA
<213> Micromonospora carbonacea

<400> 4
tattagtccg cacgccgccc ggccccgccg gagcggagcg catggtggct gtagctcagt 60
tggcagagca ccgggttgtg gtcccggttg tcgtgggttc aattcccatc agtcacccgt 120
acacgaaggc ccctccact cggaggggggc cttcggcgtt cctgagggtt cgcggtcagg 180
cggtcggctc ggcgctgggg gactcggccc cgtcggcggg agtggcctcg gcgtccgggg 240
a   241

<210> 5
<211> 243
<212> DNA
<213> Micromonospora carbonacea

<400> 5
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tggtggctgt agctcagttg gcagagcacc gggttgtggt cccggttgtc gtgggttcaa 120
ttcccatcag tcacccggca agtggatcta ctccacagca gatcaggccc cctccgaaga 180
gggggcctga tgcgtcatag gggacaggta ggggaactca accccggct ccttgctcgc 240
gtc   243

<210> 6
<211> 247
<212> DNA
<213> Micromonospora carbonacea

<400> 6
tagggggaatc cactccggag acgcccggag caatccggag catgacggag caaccagcag 60
gtcaggtggc ctgttgaccc cctgaccagg gccccggtac gggttcaatt cccatcagtc 120
acccgtacac gaaggcccccc tccactcgga ggggccttc ggcgttcctg agggttcgcg 180
gtcaggcggt cggctcggcg ctgggggact cggccccgtc ggcgggagtg gcctcggcgt 240
ccggggga   247

<210> 7
<211> 255
<212> DNA
<213> Micromonospora halophytica

<400> 7
tttctccgca cccgcccggg gcgttcgacc gggtgcggcg gcatggtggc tgtagctcag 60
ttggcagagc accgggttgt ggtcccggtt gtcgtgggtt caattcccat cagtcacccc 120

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aggtaagacc caggtcaggg ccggttctca ccggccctga cgcattttca ggggcatggt 180
gggggcgcta ccggggggtgg ggtgtctcac cgcgagccag catctcgatc aggcgatcga 240
gccggcgctg ccggg                                                   255
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<210> 8
<211> 315
<212> DNA
<213> Micromonospora halophytica
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<400> 8
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ttggcagagc accgggttgt ggtcccggtt gtcgtgggtt caattcccat cagtcacccg 120
gcaagtggat ctactccaca gcagatcagg cccccctccga agagggggcc tgatgcgtca 180
tagggggacag gtagggggaac tcaacccccg gctccttgct cgcgtcgggt catgccgtcc 240
gcgtacccct ccgcgtacct ggccctctcc cgttcctcga tctcggcggc gagctgatcg 300
cgcaggtgcg cctcc                                                   315
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<210> 9
<211> 260
<212> DNA
<213> Micromonospora halophytica
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<400> 9
tagggggaatc cactccggag acgcccggag caatccggag catgacggag caaccagcag 60
gtcaggtggc ctgttgaccc cctgaccagg gccccggtac gggttcaatt cccatcagtc 120
accccaggta agacccaggt cagggccggt tctcaccggc cctgacgcat tttcaggggc 180
atggtggggg cgctaccggg ggtggggtgt ctcaccgcga gccagcatct cgatcaggcg 240
atcgagccgg cgctgccggg                                              260
```

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<210>   10

<211>   209

<212>   DNA

<213>   artificial sequence



<220>

<223>   pMLP1 attP region

<400>   10
tagggggaatc cactccggag acgcccggag caatccggag catgacggag caaccagcag     60

gtcaggtggc ctgttgaccc cctgaccagg gccccggtac gggttcaatt cccatcagtc    120

acccggcaag tggatctact ccacagcaga tcaggcccccc tccgaagagg gggcctgatg    180

cgtcataggg gacaggtagg ggaactcaa                                      209
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<210>   11

<211>   19
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<212> DNA

<213> artificial sequence

<220>

<223> primer PR144

<400> 11
tgcttcgacg ccatcargg   19

<210> 12

<211> 20

<212> DNA

<213> artificial sequence

<220>

<223> primer PR145

<220>

<221> misc_feature

<222> (7)..(7)

<223> n is inosine (I)

<400> 12
gtggaanccg ccgaakccgc   20

<210> 13

<211> 20

<212> DNA

<213> artificial sequence

<220>

<223> primer PDH504

<400> 13
agggcaacaa gggaagcgtc   20

<210> 14

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<211>   21

<212>   DNA

<213>   artificial sequence


<220>

<223>   primer PDH505

<400>   14
ggcgggggtg tggctattat t                                          21


<210>   15

<211>   21

<212>   PRT

<213>   artificial sequence


<220>

<223>   amino acid sequence of open reading frame indicated in figures 4b
        and 4d

<400>   15

Ser Pro Asp Ala Glu Ala Thr Pro Ala Asp Gly Ala Glu Ser Pro Ser
1               5                   10                  15


Ala Glu Pro Thr Ala
            20


<210>   16

<211>   21

<212>   PRT

<213>   artificial sequence


<220>

<223>   amino acid sequence of open reading frame indicated in figures 5b
        and 5d

<400>   16

Arg Gln Arg Arg Leu Asp Arg Leu Ile Glu Met Leu Ala Arg Gly Glu
1               5                   10                  15
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Thr Pro His Pro Arg
                20